



SEQUENCE LISTING

a8
<110> Duvick, Johnathan P.

Gilliam, Jacob T.

Maddox, Joyce R.

Rao, Aragula Gururaj

Crasta, Oswald R.

Folkerts, Otto

<120> Amino Polyol Aamine Oxidase Polynucleotides and Related Polypeptides and Methods of Use

<130> 1134R

<140> US 09/658,835

<141> 2000-09-08

<150> US 60/092,936

<151> 1998-07-25

<150> US 60/135,391

<151> 1999-05-21

<150> US 09/352,159

<151> 1999-07-12

<151> 1999-07-12

<150> US 09/352,168

<151> 1999-07-12

<160> 54

<170> PatentIn version 3.1

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<213> Exophiala spinifera

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attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtca cagctcgatt 180
ggaggacgcc cgagaagcct tggcgcc accacggctt gtcccatacg aagactatct 240
tgctata tagta gcccaggata gaattttccg ccaatgcttg cttctcgccg ggaagaggtg 300
gtgaaaatgt caaggtggga tacaaggttg tcggtaacga aaccancacc ttttgcttc 360
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<211> 182

<212> DNA

<213> Exophiala spinifera

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tacaaggttg tcggtaacga aaccaccacc ttttgcttc ggaacacggc gcccgaggcc 120
gatcgtaactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc 180
ac 182

<210> 3
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<212> DNA
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<220>
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<400> 3
tggtttcgtt accgacaacc ttgttatccc 29

<210> 4
<211> 28
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<213> Artificial Sequence

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<400> 4
gagttggtcc cagacagact tttgtcgt 28

<210> 5
<211> 1389
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<213> *Exophiala spinifera*

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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65 70 75 80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85 90 95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100 105 110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc 384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
115 120 125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg 432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 135 140

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg 480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145 150 155 160

cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt 528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
165 170 175

gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag 576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
180 185 190

agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg 624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Asp Gly

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tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala 225	230	235	720
gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly 245	250	255	768
gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu 260	265	270	816
tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala 275	280	285	864
ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val 290	295	300	912
tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln 305	310	315	960
tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val 325	330	335	1008
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga ccg Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg 340	345	350	1056
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp 355	360	365	1104
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro 370	375	380	1152
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly 385	390	395	1200
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg Ala Pro Ser Ala Val Tyr Glu Leu Asn Asp Leu Ile Thr Leu Gly Ser 405	410	415	1248
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr 420	425	430	1296

tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa 1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
435 440 445

cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1389
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<210> 6

<211> 462

<212> PRT

<213> Exophiala spinifera

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35 40 45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85 90 95

Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100 105 110

Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
195 200 205

Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
210 215 220

Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
225 230 235 240

Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
245 250 255

Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
260 265 270

Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
275 280 285

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
290 295 300

Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
305 310 315 320

Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
325 330 335

Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
340 345 350

Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
355 360 365

Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
370 375 380

Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
385 390 395 400

Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
405 410 415

Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
420 425 430

Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
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<210> 7

<211> 1442

<212> DNA

<213> Exophiala spinifera

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<222> (646)..(698)

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<222> (699)..(1439)

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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65 70 75 80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85 90 95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100 105 110

gtt gca agt gca ctt gct gaa ctc ctc ccc gta tgg tct cag ctg atc 384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
115 120 125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg 432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 135 140

ctc gac agt gtg agc ttc gct cac tac tgt gag aag gaa cta aac ttg 480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145 150 155 160

cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt 528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
165 170 175

gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag 576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
180 185 190

agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg 624

405	410	415	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg acg tct Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser			1352
420	425	430	
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg			1400
435	440	445	
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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly 35 40 45			
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp 50 55 60			
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu 65 70 75 80			
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp 85 90 95			
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu 100 105 110			
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile 115 120 125			

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
195 200 205

Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
210 215 220

Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
225 230 235 240

Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
245 250 255

Ala Val Phe Arg Ser Lys Val Val Val Ser Leu Pro Thr Thr Leu
260 265 270

Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
275 280 285

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
290 295 300

Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
305 310 315 320

Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
325 330 335

Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
340 345 350

Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
355 360 365

Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
370 375 380

Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
385 390 395 400

Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
405 410 415

Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
420 425 430

Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
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<211> 458

<212> PRT

<213> Exophiala spinifera

<400> 9

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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
35 40 45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85 90 95

Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100 105 110

Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
195 200 205

Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly
210 215 220

Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met
225 230 235 240

Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro
245 250 255

Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro
260 265 270

Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln
275 280 285

Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys

290 295 300
His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr
305 310 315 320

Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn
325 330 335

Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser
340 345 350

Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly
355 360 365

Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr
370 375 380

Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg
385 390 395 400

Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu
405 410 415

Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg
420 425 430

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Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr
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<210> 10
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<212> DNA
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<222> (1)..(1389)

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 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30

 ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45

 ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60

 gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80

 gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95

 gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110

 gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125

 atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140

 cggtt gca agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160

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ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190	576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205	624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 210 215 220	672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240	720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255	768
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260 265 270	816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285	864
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gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320	960
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335	1008
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gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 375 380	1152
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt			1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag			1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt			1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag			1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
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Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val			
20	25	30	
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser			
35	40	45	
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			
50	55	60	
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			

65	70	75	80												
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
				85				90					95		
Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	
				100			105				110				
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
				115			120				125				
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
				130			135			140					
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
				145			150		155		160				
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
				165			170		175						
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
				180			185			190					
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
				195			200			205					
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
				210			215			220					
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
				225			230			235		240			
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
				245			250			255					
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
				260			265			270					
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
				275			280			285					
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
				290			295			300					

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305 310 315 320

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
450 455 460

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into expression vectors,
N23256

<400> 12
gggaaattca aagacaacgt tgccggacgtg gtag

34

<210> 13

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into expression vectors
N23256

<400> 13

ggggcggccg cctatgctgc tggcaccagg ctag

34

<210> 14

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 3' RACE, N21965

<400> 14

tggtttcgtt accgacaacc ttgttatccc

29

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 5' RACE, N21968

<400> 15

gagttggtcc cagacagact tttgtcgt

28

<210> 16
 <211> 1673
 <212> DNA
 <213> Exophiala spinifera

<220>
 <221> sig_peptide
 <222> (1)..(267)
 <223> yeast alpha mating factor secretion signal

<220>
 <221> CDS
 <222> (1)..(1662)
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 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 1 5 10 15

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa 96
 Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln
 20 25 30

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc 144
 Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
 35 40 45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg 192
 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
 50 55 60

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta 240
 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
 65 70 75 80

tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg 288
 Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
 85 90 95

gac	gtg	gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggt	ttg	gag	acg	gca	cgc		336
Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg		
100								105					110				
aaa	gtc	cag	gcc	gcc	ggt	ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat		384
Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp		
115						120					125						
cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tcg	ggt	ccc	ggc	agg	acg		432
Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr		
130						135					140						
act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc		480
Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser		
145						150				155			160				
gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag		528
Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln		
165						170					175						
agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	gac	ggt	aca	acc	act		576
Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr		
180						185					190						
aca	gct	cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca		624
Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala		
195						200				205							
ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc		672
Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser		
210						215				220							
ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cg	ctc	gac	agt	gtg		720
Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val		
225						230				235			240				
agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc		768
Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu		
245						250					255						
ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggt	gtg	gaa	gcc	cac		816
Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His		
260						265					270						
gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggt		864
Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly		
275						280					285						
ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga		912
Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg		
290						295					300						
tgc	aaa	aca	ggt	atg	cag	tcg	att	tgc	cat	gcc	atg	tca	aag	gaa	ctt		960
Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu		
305						310				315			320				
gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag		1008

Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln			
325	330	335	
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtc ttc cga			1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg			
340	345	350	
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg			1104
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu			
355	360	365	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat			1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn			
370	375	380	
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg			1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro			
385	390	395	400
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac			1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp			
405	410	415	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg			1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp			
420	425	430	
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa			1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln			
435	440	445	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca			1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala			
450	455	460	
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc			1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu			
465	470	475	480
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc			1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala			
485	490	495	
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg			1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr			
500	505	510	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg			1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp			
515	520	525	
aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca			1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala			
530	535	540	
gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c			1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala			

545

550

<210> 17

<211> 554

<212> PRT

<213> *Exophiala spinifera*

<400> 17

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
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Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
20 25 30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
35 40 45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
50 55 60

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65 70 75 80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
85 90 95

Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
100 105 110

Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
115 120 125

Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
130 135 140

Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
145 150 155 160

Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
165 170 175

Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
180 185 190

Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
195 200 205

Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
210 215 220

Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
225 230 235 240

Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
245 250 255

Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
260 265 270

Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
275 280 285

Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
290 295 300

Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
305 310 315 320

Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln
325 330 335

Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
340 345 350

Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
355 360 365

Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
370 375 380

Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
385 390 395 400

Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
405 410 415

Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
420 425 430

Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
435 440 445

Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
450 455 460

Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
465 470 475 480

Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
485 490 495

Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
500 505 510

Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
515 520 525

Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
530 535 540

Glu Val Val Ala Ser Leu Val Pro Ala Ala
545 550

<210> 18

<211> 2079

<212> DNA

<213> Unknown

<220>

<223> GST:K:trAPAO 2079 for bacterial expression

<220>

<221> CDS

<222> (1)..(2076)

<223>

<220>

<221> misc_feature

<222> (1)..(687)

<223> gst fusion + polylinker

<220>

<221> misc_feature

<222> (688)..(2076)

<223> K:trAPAO

<220>

<221> misc_feature

<222> (688)..(690)

<223> Extra lysine

<400> 18

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

48

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

96

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

144

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

192

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn

240

65	70	75	80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95				288
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser 100 105 110				336
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu 115 120 125				384
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 135 140				432
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 150 155 160				480
gtt gtt tta tac atg gac cca atg tgc gat gcg ttc cca aaa tta Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175				528
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr 180 185 190				576
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205				624
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220				672
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Gly 225 230 235 240				720
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly 245 250 255				768
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr 260 265 270				816
ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly 275 280 285				864
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe 290 295 300				912

gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser 305 310 315 320	960
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp 325 330 335	1008
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 340 345 350	1056
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala 355 360 365	1104
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys 370 375 380	1152
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile 385 390 395 400	1200
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe 405 410 415	1248
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser 420 425 430	1296
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln 435 440 445	1344
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His 450 455 460	1392
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr 465 470 475 480	1440
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val 485 490 495	1488
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu 500 505 510	1536
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr 515 520 525	1584

agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly 530 535 540	1632
ttc tcg ggc gtc ctccaa tcg agc tgt gac ccc atc tca ttt gcc aga Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg 545 550 555 560	1680
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met 565 570 575	1728
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg 580 585 590	1776
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly 595 600 605	1824
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys 610 615 620	1872
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp 625 630 635 640	1920
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His 645 650 655	1968
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly 660 665 670	2016
gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu 675 680 685	2064
gtg cca gca gca tag Val Pro Ala Ala 690	2079

<210> 19

<211> 692

<212> PRT

<213> Unknown

<220>

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<223> GST:K:trAPAO 2079  for bacterial expression

<220>

<221> misc_feature

<222> (1)..(687)

<223> gst fusion + polylinker

<220>

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<222> (688)..(2076)

<223> K:trAPAO

<220>

<221> misc_feature

<222> (688)..(690)

<223> Extra lysine

<400> 19

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
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Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20                     25                  30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35                     40                  45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50                     55                  60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                     70                  75                  80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85                     90                  95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100                    105                 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu

```

115	120	125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		
130	135	140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp		
145	150	160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu		
165	170	175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr		
180	185	190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala		
195	200	205
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg		
210	215	220
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Gly		
225	230	235
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly		
245	250	255
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr		
260	265	270
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly		
275	280	285
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe		
290	295	300
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser		
305	310	315
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp		
325	330	335
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro		
340	345	350

Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
355 360 365

Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
370 375 380

Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
385 390 395 400

Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
405 410 415

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
420 425 430

Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
435 440 445

Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
450 455 460

Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
465 470 475 480

Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
485 490 495

Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
500 505 510

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
515 520 525

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
530 535 540

Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
545 550 555 560

Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
565 570 575

Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
580 585 590

Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
595 600 605

Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
610 615 620

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
625 630 635 640

Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
645 650 655

Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
660 665 670

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
675 680 685

Val Pro Ala Ala
690

<210> 20

<211> 1464

<212> DNA

<213> Unknown

<220>

<223> K:trAPAO translational fusion with barley alpha amylase

<220>

<221> sig_peptide

<222> (1)..(72)

<223> Barley alpha amylase signal sequence

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 <223> K:trAPAO cDNA

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 <222> (73)..(75)
 <223> Added lysine residue

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1	5	10	
		15	
ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gct gac gtg gta		96	
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val			
20	25	30	
gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag		144	
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln			
35	40	45	
gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg		192	
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly			
50	55	60	
gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac		240	
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn			
65	70	75	80
gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc		288	
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser			
85	90	95	
aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act		336	
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr			

100	105	110	
gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro	115	120	384
125			
tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu	130	135	432
140			
ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp	145	150	480
155			
160			
ctc aag gcg agc cct cag gcg aag cg ^g ctc gac agt gtg agc ttc gcg Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala	165	170	528
175			
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala	180	185	576
190			
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Ala His Glu Ile Ser	195	200	624
205			
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn	210	215	672
220			
att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr	225	230	720
240			
225			
235			
240			
ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly	245	250	768
255			
245			
250			
255			
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser	260	265	816
270			
260			
265			
270			
ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys	275	280	864
285			
275			
280			
285			
gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser	290	295	912
300			
290			
295			
300			
cca cct ctt ccc gcc gag aag caa gca ttg gc ^g gaa aat tct atc ctg Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu	305	310	960
315			
320			
305			
310			
315			
320			
ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg	325	330	1008
335			
325			
330			
335			

gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca		1056	
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser			
340	345	350	
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc		1104	
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr			
355	360	365	
tgt ttc atg gtc gga gac ccg gga cg ^g aag tgg tcc caa cag tcc aag		1152	
Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys			
370	375	380	
cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag		1200	
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu			
385	390	395	400
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag		1248	
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu			
405	410	415	
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg		1296	
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly			
420	425	430	
ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag		1344	
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys			
435	440	445	
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat		1392	
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr			
450	455	460	
atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg		1440	
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val			
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gct agc ctg gtg cca gca gca tag		1464	
Ala Ser Leu Val Pro Ala Ala			
485			

<210> 21

<211> 487

<212> PRT

<213> Unknown

<220>

<223> K:trAPAO translational fusion with barley alpha amylase

<220>

<221> misc_feature
 <222> (73)..(1464)
 <223> K:trAPAO cDNA
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 <221> misc_feature
 <222> (73)..(75)
 <223> Added lysine residue
 <400> 21

Met	Ala	Asn	Lys	His	Leu	Ser	Leu	Ser	Leu	Phe	Leu	Val	Leu	Leu	Gly
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								20						25	30

Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
								35					40		45

Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
								50					55		60

Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
								65					70		75

Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser
								85					90		95

Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr
								100					105		110

Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Ala	Pro	
								115					120		125

Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu
								130					135		140

Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp
								145					150		155

Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
165 170 175

His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala
180 185 190

Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
195 200 205

Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
210 215 220

Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
225 230 235 240

Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
245 250 255

Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
260 265 270

Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys
275 280 285

Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
290 295 300

Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
305 310 315 320

Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
325 330 335

Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
340 345 350

Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
355 360 365

Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
370 375 380

Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu

385

390

395

400

Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
405 410 415

Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
420 425 430

Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
435 440 445

Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
450 455 460

Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
465 470 475 480

Ala Ser Leu Val Pro Ala Ala
485

<210> 22

<211> 1803

<212> DNA

<213> Exophiala spinifera

<220>

<221> CDS

<222> (1)..(1800)

<223>

<400> 22

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gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg 96
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg 96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
20 25 30

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct 144

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro			
35	40	45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys			
50	55	60	192
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr			
65	70	75	80
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly			
85	90	95	288
ctg aag gct acc ttt gcc ctt gac agg ctc cct tgc acg ctg gtg Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val			
100	105	110	336
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala			
115	120	125	384
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val			
130	135	140	432
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc gta gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc			
145	150	155	480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val			
160			480
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val			
165	170	175	528
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile			
180	185	190	576
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val			
195	200	205	624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr			
210	215	220	672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala			
225	230	235	720
240			
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala			
245	250	255	768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln			
			816

260	265	270	
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc			864
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc			864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe			
275	280	285	
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta			912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val			
290	295	300	
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc			960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile			
305	310	315	320
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt			1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser			
325	330	335	
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa			1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys			
340	345	350	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca			1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro			
355	360	365	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca			1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala			
370	375	380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa			1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
385	390	395	400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt			1248
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt			1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
405	410	415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc			1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
420	425	430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg			1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
435	440	445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc			1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			
450	455	460	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att			1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
465	470	475	480
acc tgt ttc atg gtc gga gac ccg gga cg aag tgg tcc caa cag tcc			1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			
485	490	495	

aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 500	505	510	1536
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 515	520	525	1584
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 530	535	540	1632
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 545	550	555	1680
560			
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 565	570	575	1728
580			
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 585	590		1776
595			
gtg gct agc ctg gtg cca gca gca tag Val Ala Ser Leu Val Pro Ala Ala 600			1803
<210> 23			
<211> 600			
<212> PRT			
<213> Exophiala spinifera			
<400> 23			
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro 1	5	10	15
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val 20	25	30	
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro 35	40	45	
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys 50	55	60	

Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65				70				75					80		
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly															
	85				90				95						
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val															
	100				105				110						
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala															
	115			120			125								
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val															
	130			135			140								
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val															
	145			150			155			160					
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val															
	165			170			175								
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile															
	180			185			190								
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val															
	195			200			205								
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr															
	210			215			220								
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala															
	225			230			235			240					
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala															
	245			250			255								
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln															
	260			265			270								
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe															
	275			280			285								

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile

515

520

525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590

Val Ala Ser Leu Val Pro Ala Ala
595 600

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ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala 20 25 30	96
ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc Gly Met Val Val Gly Thr Thr Val Pro Gly Thr Thr Ala Thr 35 40 45	144
gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe 50 55 60	192
gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr 65 70 75 80	240
gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu 85 90 95	288
cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly	336

100	105	110	
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu	115	120	384Glu Ser
125			
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu	130	135	432
140			
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala	145	150	480
155			
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu	165	170	528
175			
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly	180	185	576
190			
ttc cta gaccaa agg ttt gct ttg gat tgg gta cag cgaa acatc gca Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala	195	200	624
205			
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala	210	215	672
220			
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro	225	230	720
235			
240			
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc Pro Phe Arg Ala Ala Met Glu Ser Gly Val Ala Asn Tyr Asn Phe	245	250	768Pro Phe
255			
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Val Gln Ala Leu	260	265	816
270			
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp	275	280	864
285			
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Phe Glu	290	295	912
300			
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg	305	310	960
315			
320			
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala	325	330	1008
335			

aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat		1056	
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr			
340	345	350	
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt		1104	
Leu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu			
355	360	365	
gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag		1152Gly Ala	
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln			
370	375	380	
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc		1200	
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile			
385	390	395	400
gtg gct cag gac tcc cg ^g aat cg ^g ggt atc cct tct tgg cg ^c tac tac		1248	
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr			
405	410	415	
tac aat gc ^g acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg		1296	
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val			
420	425	430	
tac cac agc tct gaa gtc ggg atg gtg ttt ggc ac ^g tat cct gtc gca		1344	
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala			
435	440	445	
agt gc ^g acc gc ^c ttg gag gc ^c cag ac ^g ac ^g aaa tac atg cag ggt gc ^c		1392	
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala			
450	455	460	
tgg gc ^c gcc ttt gc ^c aaa aac cc ^c atg aat ggg cct ggg tgg aaa caa		1440	
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln			
465	470	475	480
gtg cc ^g aat gtc gc ^g gc ^g ctt ggc tca cca ggc aaa gc ^c atc cag gtt		1488	
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val			
485	490	495	
gac gtc tct cca gc ^g aca ata gac caa cga tgt gc ^c ttg tac ac ^g cgt		1536Asp Val	
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg			
500	505	510	
tat tat act gag ttg ggc aca atc gc ^g cc ^g agg aca ttt ggc gga ggc		1584	
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly			
515	520	525	
agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gc ^g gac gtg		1632	
Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val			
530	535	540	
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag ac ^g gca cg ^c aaa gc ^c		1680	
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val			
545	550	555	560

cag gcc gcc ggt ctg tcc tgc ctc gtt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 565 570 575	1728
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 580 585 590	1776
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 595 600 605	1824
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 610 615 620	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 625 630 635 640	1920Thr Gly
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 645 650 655	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 660 665 670	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 675 680 685	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 690 695 700	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 705 710 715 720	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 725 730 735	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 740 745 750	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 755 760 765	2304Thr Gly
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 770 775 780	2352
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa	2400

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
785	790	795	800
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt			2448
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
805	810	815	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc			2496
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
820	825	830	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg			2544
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
835	840	845	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc			2592
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			
850	855	860	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att			2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
865	870	875	880
acc tgt ttc atg gtc gga gac ccg gga aag tgg tcc caa cag tcc			2688Thr Cys
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			
885	890	895	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac			2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr			
900	905	910	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc			2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile			
915	920	925	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat			2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr			
930	935	940	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc			2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe			
945	950	955	960
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg			2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly			
965	970	975	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt			2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val			
980	985	990	
gtg gct agc ctg gtg cca gca gca tag			3003
Val Ala Ser Leu Val Pro Ala Ala			
995	1000		

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<213> unknown

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<222> (1576)..(1611)
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<222> (1612)..(3000)
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1 5 10 15

Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
20 25 30

Gly Met Val Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
35 40 45

Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
50 55 60

Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
65 70 75 80

Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
85 90 95

Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly
100 105 110

Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu
115 120 125

Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu
130 135 140

Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala
145 150 155 160

Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu
165 170 175

Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly
180 185 190

Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
195 200 205

Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala
210 215 220

Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro
225 230 235 240

Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe
245 250 255

Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu
260 265 270

Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp
275 280 285

Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu
290 295 300

Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg
305 310 315 320

Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala
325 330 335

Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr
340 345 350

Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu
355 360 365

Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln
370 375 380

Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile
385 390 395 400

Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr
405 410 415

Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val
420 425 430

Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala
435 440 445

Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala
450 455 460

Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln
465 470 475 480

Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val
485 490 495

Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg
500 505 510

Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly
515 520 525

Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val
530 535 540

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
545 550 555 560

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
565 570 575

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
580 585 590

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
595 600 605

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
610 615 620

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala
625 630 635 640

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
645 650 655

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
660 665 670

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
675 680 685

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
690 695 700

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
705 710 715 720

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser

725

730

735

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
740 745 750

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
755 760 765

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
770 775 780

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
785 790 795 800

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
805 810 815

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
820 825 830

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
835 840 845

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
850 855 860

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
865 870 875 880

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
885 890 895

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
900 905 910

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
915 920 925

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
930 935 940

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
945 950 955 960

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
965 970 975

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
980 985 990

Val Ala Ser Leu Val Pro Ala Ala
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<212> DNA

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<223> Barley alpha amylase signal sequence

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<223> spacer sequence

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<223> Extra lysine

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-20 -15 -10		
ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc		96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr		
-5 -1 1 5		
gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc		144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg		
10 15 20		
gga ata ccc tat gca gcg ccg ctc gtc ggg ctg cgt tgg aag ccg		192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro		
25 30 35 40		
ccc caa cac gcc ccg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt		240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe		
45 50 55		
ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc		288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala		
60 65 70		

ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser	75	80	85	336
ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly	90	95	100	384
ggc ttc gcc ggc ggc acg gcc atg ccc tac tac gac ggc gag gcg Gly Phe Ala Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala	105	110	115	432
ctt gcg cga cag ggc gtc gtc gtg acg ttt aac tat cgg acg aac Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn	125	130	135	480
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag acg ccc acc Ile Leu Gly Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr	140	145	150	528
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Ala Ala Leu Arg	155	160	165	576
tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val	170	175	180	624
acg gtc ttt ggt gaa tcg gcc gga gcg acg gcg atc gga ctt ctg ctc Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu	185	190	195	672
acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser	205	210	215	720
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser	220	225	230	768
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro	235	240	245	816
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp	250	255	260	864
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu	265	270	275	912
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val	285	290	295	960
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg				1008

Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly			
300	305	310	
cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg			1056
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala			
315	320	325	
cag ttt ggc gac caa gcc gcc gtg gcg gcg tgc tat ccc ctc gac			1104
Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp			
330	335	340	
ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat			1152
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn			
345	350	355	360
cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag			1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln			
365	370	375	
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga			1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly			
380	385	390	
aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg			1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val			
395	400	405	
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc			1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro			
410	415	420	
acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc			1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val			
425	430	435	440
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct			1440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro			
445	450	455	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc			1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg			
460	465	470	
gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc			1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly			
475	480	485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc			1584
Ala Lys Ala Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser			
490	495	500	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt			1632
Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly			
505	510	515	520
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt			1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val			

525	530	535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 540	545	550	1728
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 555	560	565	1776
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 570	575	580	1824
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 585	590	595	1872
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 605	610	615	1920
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 620	625	630	1968
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 635	640	645	2016
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 650	655	660	2064
ttg cct gct ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 665	670	675	2112
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 685	690	695	2160
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 700	705	710	2208
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 715	720	725	2256
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 730	735	740	2304
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 745	750	755	2352
			760

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 765 770 775	2400
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 780 785 790	2448
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 795 800 805	2496
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 810 815 820	2544
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 825 830 835 840	2592
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 845 850 855	2640
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 860 865 870	2688
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 875 880 885	2736
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 890 895 900	2784
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 905 910 915 920	2832
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 925 930 935	2880
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 940 945 950	2928
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 955 960 965	2976

<210> 27

<211> 991

<212> PRT

<213> Unknown

<220>

<223> Barley alpha amylase signal sequence:BEST1 mature:artificial spacer:K:trAPAO

<220>

<221> misc_feature

<222> (1546)..(1584)

<223> spacer sequence

<220>

<221> misc_feature

<222> (1585)..(2973)

<223> K:trAPAO

<220>

<221> misc_feature

<222> (1585)..(1587)

<223> Extra lysine

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
-20 -15 -10

Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
-5 -1 1 5

Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
10 15 20

Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
25 30 35 40

Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
45 50 55

Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
60 65 70

Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
75 80 85

Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
90 95 100

Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala
105 110 115 120

Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn
125 130 135

Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr
140 145 150

Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg
155 160 165

Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val
170 175 180

Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu
185 190 195 200

Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser
205 210 215

Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser
220 225 230

Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro
235 240 245

Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp
250 255 260

Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu
265 270 275 280

Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val
285 290 295

Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly
300 305 310

Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala
315 320 325

Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp
330 335 340

Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn
345 350 355 360

Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln
365 370 375

Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly
380 385 390

Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val
395 400 405

Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro
410 415 420

Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val
425 430 435 440

Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro
445 450 455

Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg
460 465 470

Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly
475 480 485

Ala Lys Ala Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser
490 495 500

Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly

505	510	515	520
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val			
525		530	535
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser			
540		545	550
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			
555		560	565
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			
570		575	580
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln			
585		590	595
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			
605		610	615
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
620		625	630
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
635		640	645
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
650		655	660
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
665		670	675
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
685		690	695
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
700		705	710
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala			
715		720	725
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
730		735	740

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
745 750 755 760

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
765 770 775

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
780 785 790

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
795 800 805

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
810 815 820

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825 830 835 840

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
845 850 855

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
860 865 870

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
875 880 885

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
890 895 900

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
905 910 915 920

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
925 930 935

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
940 945 950

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
955 960 965

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<210> 28

<211> 3618

<212> DNA

<213> Unknown
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<220>

<223> gst:esp1:sp:K:trAPAO

<220>

<221> CDS

<222> (1)..(3615)

<223>
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<220>

<221> misc_feature

<222> (1)..(687)

<223> gst + polylinker
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<220>

<221> mat_peptide

<222> (688)..()

<223> esp1 mat
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<221> misc_feature

<222> (2191)..(2226)

<223> spacer sequence
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<221> misc_feature
<222> (2227)..(3615)
<223> K:trAPAO

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<222> (2227)..(2229)
<223> extra lysine

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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln
          -225           -220           -215

ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag      90
Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
          -210           -205           -200

cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag      135
His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys
          -195           -190           -185

ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat      180
Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
          -180           -175           -170

ggg gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata      225
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile
          -165           -160           -155

gct gac aag cac aac atg ttg ggt ggt tgt cca aaa gag cgt gca      270
Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala
          -150           -145           -140

gag att tca atg ctt gaa gga gcg gtt ttg gat att aga tac ggt      315
Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly
          -135           -130           -125

gtt tcg aga att gca tat agt aaa gac ttt gaa act ctc aaa gtt      360
Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val
          -120           -115           -110

gat ttt ctt agc aag cta cct gaa atg ctg aaa atg ttc gaa gat cgt      408
Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg
          -105           -100           -95

tta tgt cat aaa aca tat tta aat ggt gat cat gta acc cat cct gac      456
Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp

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	-90	-85	-80	
ttc atg ttg tat gac gct ctt gat gtt gtt tta tac atg gac cca atg Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met	-75	-70	-65	504
tgc ctg gat gcg ttc cca aaa tta gtt tgt ttt aaa aaa cgt att gaa Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu	-60	-55	-50	552
gct atc cca caa att gat aag tac ttg aaa tcc agc aag tat ata gca Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala	-45	-40	-35	600
tgg cct ttg cag ggc tgg caa gcc acg ttt ggt ggt ggc gac cat cct Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Asp His Pro	-25	-20	-15	648
cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gaa ttc gct cct act Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Ala Pro Thr	-10	-5	-1 1	696
gtc aag att gat gct ggg atg gtg gtc ggc acg act act act gtc ccc Val Lys Ile Asp Ala Gly Met Val Val Gly Thr Thr Thr Thr Val Pro	5	10	15	744
ggc acc act gcg acc gtc acg gag ttc ttg ggc gtt cct ttt gcc gcc Gly Thr Thr Ala Thr Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala	20	25	30 35	792
tct ccg aca cga ttt gcg cct act cgt ccc gtg cct tgg tca acg Ser Pro Thr Arg Phe Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr	40	45	50	840
cct ttg caa gcc act gca tat ggt cca gca tgc cct caa caa ttc aat Pro Leu Gln Ala Thr Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn	55	60	65	888
tac ccc gaa gaa ctc cgt gag att acg atg gcc tgg ttc aat aca ccg Tyr Pro Glu Glu Leu Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro	70	75	80	936
ccc ccg tca gct ggt gaa agt gag gac tgc ctg aac ctc aac atc tac Pro Pro Ser Ala Gly Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr	85	90	95	984
gtc cca gga act gag aac aca aac aaa gcc gtc atg gtt tgg ata tac Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr	100	105	110 115	1032
ggt gga gcg ctg gaa tat ggt tgg aat tca ttc cac ctt tac gac ggg Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly	120	125	130	1080
gct agt ttc gca gcc aat cag gat gtc atc gcc gtg acc atc aac tac Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr	135	140	145	1128

aga acg aac att ctg ggg ttc cct gct gcc cct cag ctt cca ata aca Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr 150 155 160	1176
cag cga aat ctg ggg ttc cta gac caa agg ttt gct ttg gat tgg gta Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val 165 170 175	1224
cag cgg aac atc gca gcc ttt ggc ggt gat cct cga aag gtc aca ata Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile 180 185 190 195	1272
ttt ggg cag agt gcg ggg ggc aga agt gtc gac gtc ctc ttg acg tct Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser 200 205 210	1320
atg cca cac aac cca ccc ttc cga gca gca atc atg gag tcc ggt gtg Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val 215 220 225	1368
gct aac tac aac ttc ccc aag gga gat ttg tcc gaa cct tgg aac acc Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr 230 235 240	1416
act gtt caa gct ctc aac tgt acc acc agt atc gac atc ttg agt tgt Thr Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys 245 250 255	1464
atg aga aga gtc gat ctc gcc act ctg atg aac acg atc gag caa ctc Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu 260 265 270 275	1512
gga ctt ggg ttt gag tac acg ttg gac aac gta acg gct gtg tac cgt Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg 280 285 290	1560
tct gaa acg gct cgc acg act ggt gac att gct cgt gta cct gtt ctc Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu 295 300 305	1608
gtc ggg acg gtg gcc aac gac gga ctt ctc ttt gtc ctc ggg gag aat Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn 310 315 320	1656
gac acc caa gca tat ctc gag gag gca atc ccg aat cag ccc gac ctt Asp Thr Gln Ala Tyr Leu Glu Ala Ile Pro Asn Gln Pro Asp Leu 325 330 335	1704
tac cag act ctc ctt gga gca tat ccc att gga tcc cca ggg atc gga Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly 340 345 350 355	1752
tcg cct caa gat cag att gcc gcc att gag acc gag gta aga ttc cag Ser Pro Gln Asp Gln Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln 360 365 370	1800

tgt cct tct gcc atc gtg gct cag gac tcc cg ^g aat cg ^g ggt atc cct Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro 375 380 385	1848
tct tgg cgc tac tac tac aat gc ^g acc ttt gag aat ctg gag ctt ttc Ser Trp Arg Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe 390 395 400	1896
cct ggg tcc gaa gtg tac cac agc tct gaa gtc ggg atg gtg ttt ggc Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly 405 410 415	1944
acg tat cct gtc gca agt gc ^g acc gc ^c ttg gag gc ^c cag acg agc aaa Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys 420 425 430 435	1992
tac atg cag ggt gc ^c tgg gc ^g gc ^c ttt gc ^c aaa aac ccc atg aat ggg Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly 440 445 450	2040
cct ggg tgg aaa caa gtg cc ^g aat gtc gc ^g gc ^g ctt ggc tca cca ggc Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly 455 460 465	2088
aaa gcc atc cag gtt gac gtc tct cca gc ^g aca ata gac caa cga tgt Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys 470 475 480	2136
gcc ttg tac acg cgt tat tat act gag ttg ggc aca atc gc ^g cc ^g agg Ala Leu Tyr Thr Arg Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg 485 490 495	2184
aca ttt ggc gga ggc agc gc ^c gga ggc agc gc ^c gga ggc agc aaa gac Thr Phe Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Asp 500 505 510 515	2232
aac gtt gc ^g gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu 520 525 530	2280
acg gca cgc aaa gtc cag gc ^c gc ^c ggt ctg tcc tgc ctc gtt ctt gag Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu 535 540 545	2328
gc ^g atg gat cgt gta ggg gga aag act ctg agc gta caa tc ^g ggt cc ^c Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro 550 555 560	2376
ggc agg acg act atc aac gac ctc gc ^c gct gc ^g tgg atc aat gac agc Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser 565 570 575	2424
aac caa agc gaa gta tcc aga ttg ttt gaa aga tt ^t cat ttg gag gc ^c Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly 580 585 590 595	2472
gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt	2520

Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly			
600	605	610	
aca acc act aca gct tat ggt gac tcc ttg ctg agc gag gag gtt			2568
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val			
615	620	625	
gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa			2616
Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu			
630	635	640	
gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cg ^g ctc			2664
Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu			
645	650	655	
gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct			2712
Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro			
660	665	670	675
gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg			2760
Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val			
680	685	690	
gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt			2808
Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser			
695	700	705	
gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag			2856
Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln			
710	715	720	
tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca			2904
Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser			
725	730	735	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa			2952
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu			
740	745	750	755
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc			3000
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala			
760	765	770	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat			3048
Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr			
775	780	785	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg			3096
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu			
790	795	800	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg			3144
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp			
805	810	815	
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg			3192
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser			

820	825	830	835	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat				3240
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp				
840	845	850		
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cg aag				3288
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys				
855	860	865		
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa				3336
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln				
870	875	880		
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc				3384
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala				
885	890	895		
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct				3432
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala				
900	905	910	915	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg				3480
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala				
920	925	930		
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct				3528
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser				
935	940	945		
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga				3576
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg				
950	955	960		
tgt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag				3618
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala				
965	970	975		

<210> 29

<211> 1205

<212> PRT

<213> Unknown

<220>

<223> gst:esp1:sp:K:trAPAO

<220>

<221> misc_feature

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<222> (1)..(687)

<223> gst + polylinker

<220>

<221> misc_feature

<222> (2191)..(2226)

<223> spacer sequence

<220>

<221> misc_feature

<222> (2227)..(3615)

<223> K:trAPAO

<220>

<221> misc_feature

<222> (2227)..(2229)

<223> extra lysine

<400> 29

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln
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Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
      -210           -205                   -200

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys
      -195           -190                   -185

Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
      -180           -175                   -170

Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile
      -165           -160                   -155

Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala
      -150           -145                   -140

Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly
      -135           -130                   -125

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Val	Ser	Arg	Ile	Ala	Tyr	Ser	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	
-120										-115				-110	
Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg
-105									-100					-95	
Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	Gly	Asp	His	Val	Thr	His	Pro	Asp
-90									-85					-80	
Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	Val	Val	Leu	Tyr	Met	Asp	Pro	Met
-75									-70					-65	
Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu
-60						-55					-50				
Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala
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Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro
-25								-20					-15		
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-10								-5					-1	1	
Val	Lys	Ile	Asp	Ala	Gly	Met	Val	Val	Gly	Thr	Thr	Thr	Thr	Val	Pro
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Gly	Thr	Thr	Ala	Thr	Val	Ser	Glu	Phe	Leu	Gly	Val	Pro	Phe	Ala	Ala
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Ser	Pro	Thr	Arg	Phe	Ala	Pro	Pro	Thr	Arg	Pro	Val	Pro	Trp	Ser	Thr
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Pro	Leu	Gln	Ala	Thr	Ala	Tyr	Gly	Pro	Ala	Cys	Pro	Gln	Gln	Phe	Asn
55								60					65		
Tyr	Pro	Glu	Glu	Leu	Arg	Glu	Ile	Thr	Met	Ala	Trp	Phe	Asn	Thr	Pro
70							75						80		
Pro	Pro	Ser	Ala	Gly	Glu	Ser	Glu	Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr
85													95		

Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr
100 105 110 115

Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly
120 125 130

Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr
135 140 145

Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr
150 155 160

Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val
165 170 175

Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile
180 185 190 195

Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser
200 205 210

Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val
215 220 225

Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr
230 235 240

Thr Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys
245 250 255

Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu
260 265 270 275

Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg
280 285 290

Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu
295 300 305

Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn
310 315 320

Asp Thr Gln Ala Tyr Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu

325	330	335
		Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly
		340 345 350 355
		Ser Pro Gln Asp Gln Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln
	360	365 370
		Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro
		375 380 385
		Ser Trp Arg Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe
		390 395 400
		Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly
	405 410	415
		Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys
	420 425	430 435
		Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly
	440	445 450
		Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly
	455	460 465
		Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys
	470	475 480
		Ala Leu Tyr Thr Arg Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg
	485	490 495
		Thr Phe Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Asp
	500	505 510 515
		Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu
	520	525 530
		Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu
	535	540 545
		Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro
	550	555 560

Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser
Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser
565 570 575

Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly
Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly
580 585 590 595

Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly
Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly
600 605 610

Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val
615 620 625

Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu
Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu
630 635 640

Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu
Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu
645 650 655

Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro
Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro
660 665 670 675

Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val
Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val
680 685 690

Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser
Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser
695 700 705

Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln
Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln
710 715 720

Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser
Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser
725 730 735

Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu
740 745 750 755

Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala
760 765 770

Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr
775 780 785

Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu
790 795 800

Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp
805 810 815

Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser
820 825 830 835

Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp
840 845 850

Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys
855 860 865

Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln
870 875 880

Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala
885 890 895

Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala
900 905 910 915

Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala
920 925 930

Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser
935 940 945

Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg
950 955 960

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965 970 975

<210> 30

<211> 3591

<212> DNA

<213> Unknown

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      on vector pGEX-4T-1

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<221> misc_feature

<222> (1)..(687)

<223> gst + polylinker


<220>

<221> mat_peptide

<222> (688)..()

<223> BEST1 mature


<220>

<221> misc_feature

<222> (2164)..(2199)

<223> spacer sequence


<220>

<221> misc_feature

<222> (2200)..(3588)

<223> K:trAPAO


<220>

<221> CDS

<222> (1)..(3588)

<223>
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<220>

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<223> extra lysine

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ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag	90	
Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu		
-210	-205	-200
cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag	135	
His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys		
-195	-190	-185
ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat	180	
Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp		
-180	-175	-170
ggt gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata	225	
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile		
-165	-160	-155
gct gac aag cac aac atg ttg ggt ggt tgt cca aaa gag cgt gca	270	
Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala		
-150	-145	-140
gag att tca atg ctt gaa gga gcg gtt ttg gat att aga tac ggt	315	
Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly		
-135	-130	-125
gtt tcg aga att gca tat agt aaa gac ttt gaa act ctc aaa gtt	360	
Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val		
-120	-115	-110
gat ttt ctt agc aag cta cct gaa atg ctg aaa atg ttc gaa gat cgt	408	
Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg		
-105	-100	-95
tta tgt cat aaa aca tat tta aat ggt gat cat gta acc cat cct gac	456	
Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp		
-90	-85	-80
ttc atg ttg tat gac gct ctt gat gtt tta tac atg gac cca atg	504	
Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met		
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Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu		

-60	-55	-50	
gct atc cca caa att gat aag tac ttg aaa tcc agc aag tat ata gca Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala	-45	-40	600
	-35	-30	
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		-15	
cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gaa ttc acg gat ttt Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Thr Asp Phe	-10	-5	696
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		15	
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ctg cgt tgg aag ccg ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc Leu Arg Trp Lys Pro Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg	40	45	840
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		110	115
tac gac ggc gag gcg ctt gcg cga cag ggc gtc gtc gtg acg ttt Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Thr Phe	120	125	1080
		130	
aac tat cgg acg aac atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser	135	140	1128
		145	
cgc gag agc ccc acc gga act tcg ggc aac tac ggc cta ctc gac att Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile	150	155	1176
		160	
ctc gcc gct ctt cgg tgg gtg cag agc aac gcc cgc gcc ttc gga ggg Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly	165	170	1224
		175	

gac ccc ggc cga gtg acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala 180 185 190 195	1272
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gct atc ctc gaa aat cca ggg ctg acg cga ccg ctc gcg acg ctc gcc Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala 215 220 225	1368
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aat acc gag ggt gga aga gcg ccg gct acc cac gga gcc gaa att ccc Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro 390 395 400	1896

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ccg ccc gag ggg ccc acg ccc gcc gac cgt gcg ctg ggc caa ctg atg Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met 420 425 430 435	1992
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gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly 520 525 530	2280
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr 535 540 545	2328
ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly 550 555 560	2376
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe 565 570 575	2424
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser 580 585 590 595	2472
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp 600 605 610	2520
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 615 620 625	2568
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg	2616

Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala			
630	635	640	
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt			2664
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys			
645	650	655	
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc			2712
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile			
660	665	670	675
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt			2760
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe			
680	685	690	
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg			2808
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser			
695	700	705	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag			2856
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln			
710	715	720	
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac			2904
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His			
725	730	735	
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca			2952
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr			
740	745	750	755
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt			3000
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val			
760	765	770	
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt			3048
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu			
775	780	785	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat			3096
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr			
790	795	800	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc			3144
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly			
805	810	815	
ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga			3192
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg			
820	825	830	835
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg			3240
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met			
840	845	850	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga			3288
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg			

855	860	865	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly			3336
870	875	880	
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys			3384
885	890	895	
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp			3432
900	905	910	915
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His			3480
920	925	930	
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly			3528
935	940	945	
gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu			3576
950	955	960	
gtg cca gca gca tag Val Pro Ala Ala			3591
965			

<210> 31

<211> 1196

<212> PRT

<213> Unknown

<220>

<223> Open reading frame of BEST1:K:trAPAO fusion for bacterial expression vector pGEX-4T-1

<220>

<221> misc_feature

<222> (1)..(687)

<223> gst + polylinker

<220>

<221> misc_feature

<222> (2164)..(2199)
 <223> spacer sequence
 <220>
 <221> misc_feature
 <222> (2200)..(3588)
 <223> K:trAPAO
 <220>
 <221> misc_feature
 <222> (2200)..(2202)
 <223> extra lysine
 <400> 31

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	
															-215
															-225

Pro	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	
															-200
															-210

His	Leu	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	
															-185
															-195

Phe	Glu	Leu	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	
															-170
															-180

Gly	Asp	Val	Lys	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	
															-155
															-165

Ala	Asp	Lys	His	Asn	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	
															-140
															-150

Glu	Ile	Ser	Met	Leu	Glu	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	
															-125
															-135

Val	Ser	Arg	Ile	Ala	Tyr	Ser	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	
															-110
															-120

Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg
															-95
															-105

Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp
-90 -85 -80

Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met
-75 -70 -65

Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu
-60 -55 -50

Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala
-45 -40 -35 -30

Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro
-25 -20 -15

Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Thr Asp Phe
-10 -5 -1 1

Pro Val Arg Arg Thr Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp
5 10 15

Val Met Ser Phe Arg Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly
20 25 30 35

Leu Arg Trp Lys Pro Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg
40 45 50

Pro Ala Thr Gln Phe Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg
55 60 65

Lys Gly Ser Leu Ala Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn
70 75 80

Val Trp Ala Pro Ser Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val
85 90 95

Trp Val Tyr Gly Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr
100 105 110 115

Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Val Thr Phe
120 125 130

Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser
135 140 145

Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile
150 155 160

Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly
165 170 175

Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala
180 185 190 195

Ile Gly Leu Leu Leu Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly
200 205 210

Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala
215 220 225

Asp Ser Ala Ala Ser Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu
230 235 240

Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg
245 250 255

Pro Ala Ser Arg Asp Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val
260 265 270 275

Asp Gly His Val Leu Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly
280 285 290

Gln Leu Ala Pro Val Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly
295 300 305

Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln
310 315 320

Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala
325 330 335

Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg
340 345 350 355

Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu
360 365 370

Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly
375 380 385

Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro
390 395 400

Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp
405 410 415

Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met
420 425 430 435

Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp
440 445 450

Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe
455 460 465

Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro
470 475 480

Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Gly Ser Gly Gly Gly
485 490 495

Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val Gly
500 505 510 515

Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
520 525 530

Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
535 540 545

Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
550 555 560

Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
565 570 575

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser

580	585	590	595
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp			
600	605	610	
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro			
615	620	625	
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala			
630	635	640	
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys			
645	650	655	
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile			
660	665	670	675
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe			
680	685	690	
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser			
695	700	705	
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln			
710	715	720	
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His			
725	730	735	
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr			
740	745	750	755
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val			
760	765	770	
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu			
775	780	785	
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr			
790	795	800	
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly			
805	810	815	

Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
820 825 830 835

Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
840 845 850

Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
855 860 865

Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
870 875 880

Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
885 890 895

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
900 905 910 915

Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
920 925 930

Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
935 940 945

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
950 955 960

Val Pro Ala Ala
965

<210> 32

<211> 1803

<212> DNA

<213> Unknown

<220>

<223> Glyc(-) APAO coding sequence; mutation in putative glycosylation sites

<220>

<221> CDS

<222> (1)..(1803)

<223>

<400>	32	
atg gca ctt gca ccg agc tac atc aat ccc cca aac gtc gcc tcc cca		48
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro		
1	5	10
		15
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg		96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Arg Tyr Val		
20	25	30
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct		144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro		
35	40	45
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc		192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys		
50	55	60
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac		240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr		
65	70	75
		80
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg		288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly		
85	90	95
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg		336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val		
100	105	110
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc		384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala		
115	120	125
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg		432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val		
130	135	140
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc		480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val		
145	150	155
		160
cag gcc gcc ggt ctg tcc ctc gtt ctt gag gcg atg gat cgt gta		528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val		
165	170	175
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc		576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile		

180	185	190	
aac gac ctc ggc gct gcg tgg atc aat gat agc aat cag gcc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val 195	200	205	624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210	215	220	672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 225	230	235	720
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245	250	255	768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260	265	270	816
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275	280	285	864
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290	295	300	912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305	310	315	960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325	330	335	1008
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340	345	350	1056
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 355	360	365	1104
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 370	375	380	1152
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 385	390	395	1200
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 405	410	415	1248

tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 420 425 430	1296
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 435 440 445	1344
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450 455 460	1392
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 465 470 475 480	1440
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 485 490 495	1488
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 500 505 510	1536
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 515 520 525	1584
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 530 535 540	1632
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 545 550 555 560	1680
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 565 570 575	1728
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 580 585 590	1776
gtg gct agc ctg gtg cca gca gca tag Val Ala Ser Leu Val Pro Ala Ala 595 600	1803

<210> 33

<211> 600

<212> PRT

<213> Unknown

<220>

<223> Glyc(-) APAO coding sequence; mutation in putative glycosylation sites

<400> 33

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala
225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590

Val Ala Ser Leu Val Pro Ala Ala
595 600

<210> 34

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> 37-mer oligonucleotide

<400> 34 ggggaattca tggcacttgc accgagctac atcaatc 37

<210> 35

<211> 1929

<212> DNA

<213> Exophiala spinifera

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1186)

<223>

<400> 35 atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc agggtattcc 60
 cacatcgccg taggccccaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa 120
 gacgctttgg gcgtgacaga cccagcctac gagaaacagg ttgccccagc attcgccaat 180
 ctgcgagctt gccttgctgc agttggagcc tcttcaaacg acgtcaccaa gctcaattac 240
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ccgttcaagt	gtgttcattt	cgttggaaacg	gagacgtctt	tagttggaa	agggtatatg	1800
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gcagcatag						1929

<210> 36

<211> 600

<212> PRT

<213> *Exophilia spinifera*

<400> 36

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
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Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala
225 230 235 240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
260 265 270

Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
275 280 285

Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
325 330 335

Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
370 375 380

Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp

435

440

445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545 550 555 560

Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590

Val Ala Ser Leu Val Pro Ala Ala
595 600

<210> 37

<211> 1929

<212> DNA

<213> Exophiala spinifera

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1186)

<223>

<400> 37	
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gacgcggcgttgg gcgtgacaga cccagcctac gagaaacagg ttgcccaagc attgc当地	180
ctgcgagctt gccttgctgc agttggagcc tcttcaaacg acgtcaccaa gctcaattac	240
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tttgc当地tttgc acaggctccc tccttgcacg ctgggtccag taccggcctt ggcttc当地	360
gaataccctct ttgagggttga cgccacggcg ctgggtccag gacactcgac cccagacaac	420
gttgc当地ggacg tggtagtggt gggcgctggc ttgagcggct tggagacggc acgcaaagtc	480
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ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgc当地ggatc	600
aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttc当地ttt ggagggcgag	660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtaacaac cactacagct	720
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agaatacagt cactgactcc acttcgtcca gctgagcggag gaggttgc当地a gtgc当地ttgc	840
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cggtgtc当地t ctaggttaggg gactcgatcc tt当地gttgtca ttccaggtat cagtc当地gatt	1200

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ccgttcaagt	gtgttcattt	cgttggAACG	gagacgtctt	tagttggaa	agggtatatg	1860
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gcagcatag						1929

<210> 38

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 38

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val
									20			25			30

Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro
									35			40			45

Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
									50			55			60

Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
									65			70			80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala
225 230 235 240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
260 265 270

Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
275 280 285

Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
325 330 335

Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
370 375 380

Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545 550 555 560

Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590

Val Ala Ser Leu Val Pro Ala Ala
595 600

<210> 39

<211> 1930

<212> DNA

<213> *Exophiala spinifera*

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1187)

<223>

<220>

<221> misc_feature

<222> (649)..(649)

<223> n = A,T,C or G

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tgggtcg	tcaggtgggg	gactcgtttc	tcaagtggc	atttcaggta	tgcagtcgtat	1200
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aagcaaaaaa	gtgggtgttt	cgttaccgac	aacctgtat	cccaccttga	cattttcacc	1380
acctctcccc	gccgagaagc	aagcattggc	ggaaaattct	atcctggct	actatagcaa	1440
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gccgttcaag agtgttcatt tcgttggaac ggagacgtct ttagttgga aagggtatat 1860
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<210> 40

<211> 598

<212> PRT

<213> Exophiala spinifera

<220>

<221> MISC_FEATURE

<222> (216)..(216)

<223> Xaa = any amino acid

<400> 40

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Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly

85

90

95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
145 150 155 160

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
165 170 175

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
195 200 205

Arg Leu Phe Glu Arg Phe His Xaa Glu Gly Glu Leu Gln Arg Thr Thr
210 215 220

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro
225 230 235 240

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
245 250 255

Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
260 265 270

Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
275 280 285

His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn
290 295 300

Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
305 310 315 320

Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
325 330 335

Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
340 345 350

Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
355 360 365

Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
370 375 380

Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val
385 390 395 400

Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro
405 410 415

Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly
420 425 430

Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu
435 440 445

Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe
450 455 460

Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys
465 470 475 480

Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln
485 490 495

Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn
500 505 510

Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp
515 520 525

Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu
530 535 540

Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser
545 550 555 560

Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met
565 570 575

Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala
580 585 590

Ser Leu Val Pro Ala Ala
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<210> 41

<211> 1928

<212> DNA

<213> Rhinocladiella atrovirens

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1185)

<223>

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tgggtttctc tcagtgggag actcggtttctt tagtggtcat tccaggtatg cagtcgtt	1200
gccatgccat gtcaaaggaa ctgtttccag gctcagtgca cctcaacacc cccgtcgccg	1260
aaattgagca gtcggcatcc ggctgtacag tacgatcgcc ctggcgccgt gtgttccgaa	1320
gtaaaaaggt ggtggtttcg ttaccgacaa cttgttatcc caccttgata ttttaccac	1380
ctcttcccgcc cgagaagcaa gcattggctt aaaaatccat cctggctac tatacgaa	1440
tagtcttcgtt atgggacaag ccgtgggtggc gcgaacaagg cttctcgccgtt gtccctcaat	1500
cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtcgtt cggcaatgg	1560
ccattacctt tttcatggtc ggagacccgg gacggaaatgtt gtcccaacag tccaaacgg	1620
tacgacagaa gtctgtctgg aaccaactcc gcgcagccta cgagaacgcc gggggcccaag	1680
tcccagagcc ggccaaacgtt ctgcagatcg agtggtcgaa gcagcgttat ttccaaaggag	1740
cggcgagcgt cgtctatggg ctgaactgtc tcaacacactt ggggtcgccg ctcagaacgc	1800
cgttcaagggt tggttcatcc gttggaaacgg agacgtttt ggtttggaaa gggtatatgg	1860
aaggggccat acgatcggtt cagcgaggcg ctgcagaatgt tgcgttagc ctgggtgccag	1920
cagcatag	1928

<210> 42

<211> 598

<212> PRT

<213> Rhinocladiella atrovirens

<400> 42

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Ala
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60 80

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205

Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
210 215 220

Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr
225 230 235 240

Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu
245 250 255

Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro
260 265 270

Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His
275 280 285

Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn
290 295 300

Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
305 310 315 320

Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
325 330 335

Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
340 345 350

Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
355 360 365

Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
370 375 380

Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val
385 390 395 400

Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro

405

410

415

Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Leu Gly
420 425 430

Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu
435 440 445

Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe
450 455 460

Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile Thr Cys
465 470 475 480

Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln
485 490 495

Val Arg Gln Lys Ser Val Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn
500 505 510

Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp
515 520 525

Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Val Val Tyr Gly Leu
530 535 540

Asn Cys Leu Asn Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Gly
545 550 555 560

Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met
565 570 575

Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala
580 585 590

Ser Leu Val Pro Ala Ala
595

<210> 43

<211> 1928

<212> DNA

<213> Rhinocladiella atrovirens

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1186)

<223>

<400> 43
atggcacttg caccgagcta catcaatccc ccaaacctcg cctccccagc agggtattcc 60
tacgtcggcg taggccaaa cgaggaggagg tatgtgacaa tagctggaca gattggacaa 120
gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgcccagc attcgccaac 180
ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac 240
tacatcgctcg actacaaccc gagcaaactc accgcaattg gagatggct gaaggctacc 300
tttgccttg acaggctccc tccttgacag ctggtgccag tgccggccct ggcttcacct 360
gaataacctct ttgaggttga tgccacggcg ctggttccag gacactcaac cccagacaat 420
gttgcggacg tggcgttgtt gggcgctggc ttgagcgggtt tggagacggc acgcaaagtc 480
caggctgccc ggctgtcctg cctcggttctt gaggcgatgg atcgtgtggg gggaaagact 540
ctgagcgtac aatcggtcc cggcaggacg actatcaatg acctcgccgc tgcgtggatc 600
aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag 660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720
ccttatggtg attccctgggt aagcacaatt ccatttgtg atgagacctc tgtcgtgtgt 780
agaatacagt cgctgactcc acatcggtcc gctgagcggag gaggttgcaa gtgcactcgc 840
ggaactcctt cccgcatggt ctcagctgat cgaagagcat agtcttgaag accccaaggc 900
gagccctcaa gcgaagcggc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960

aaacttgcct	gctgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcggtgtgga	1020
agccccacgag	atcagcatgt	tttttctcac	cgactacatc	aagagtgccca	ccggctctcag	1080
taatattgtc	tcggataaga	aagacggtg	gcagtatatg	cgtgcgtaaa	cagggtgcgtg	1140
tggtgttctc	tca	actcggttct	tagtggtcat	tccaggtatg	cagtcgtt	1200
gccatgccat	gtcaaaggaa	cttggccag	gctcagtgc	cctcaacacc	cccgtcgccg	1260
aaattgagca	gtcggcatcc	ggctgtacag	tacgatcggc	ctcggcggc	gtgttccgaa	1320
gtaaaaaggt	ggtggtttcg	ttaccgacaa	ccttgatcc	caccttgata	ttttcaccac	1380
ctcttcccgc	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagtcttcgt	atgggacaag	ccgtgggtggc	gcgaacaagg	cttctcgcc	gtcctccaat	1500
c	cgagctgtga	ccccatctca	tttgcagag	ataccagcat	cgaagtcgt	1560
ccattacctg	tttcatggtc	ggagacccgg	gacgaaagt	gtcccaacag	tccaagcagg	1620
ta	tgacagagaa	gtctgtctgg	aaccaactcc	g	cgagaacgc	1680
tcccagagcc	ggccaaacgt	ctcgagatcg	agtggtcgaa	gcagcagtat	ttccaaggag	1740
cgccgagcgc	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaaggg	tgttcatttc	gttggAACGG	agacgtctt	ggttggaaa	gggtatatgg	1860
aaggggccat	acgatcggt	cagcgaggcg	ctgcagaagt	tgtggctagc	ctgggtccag	1920
cagcatag						1928

<210> 44

<211> 591

<212> PRT

<213> Rhinocladiella atrovirens

<400> 44

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	L	Ala	Ser	Pro
1									5			10			15

Ala	Gly	Tyr	Ser	Tyr	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Val
20									25						30

Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro
35									40						45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys
195 200 205

Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
210 215 220

Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr
225 230 235 240

Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
245 250 255

Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala
260 265 270

Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys
275 280 285

Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg
290 295 300

Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr
305 310 315 320

Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys
325 330 335

Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu
340 345 350

Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn
355 360 365

Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg
370 375 380

Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr
385 390 395 400

Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
405 410 415

Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
420 425 430

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
435 440 445

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu
450 455 460

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
465 470 475 480

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
485 490 495

Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
500 505 510

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
515 520 525

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
530 535 540

Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
545 550 555 560

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
565 570 575

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
580 585 590

<210> 45

<211> 1928

<212> DNA

<213> Rhinocladiella atrovirens

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1185)

<223>

<400> 45
atggcacttg caccgagcta catcaatcccc ccaaacctcg cctcccccagc agggtattcc 60

cacgtcggcg taggccaaa cgagggagg tatgtgaca tagctggaca gattggacaa	120
gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgccaagc attgc当地	180
ctgcgagctt gtcttgctgc agttggagcc acttcaaaccg acattaccaa gctcaattac	240
tacatcgtcg actacaaccc gagcaaactc accgcaattt gagatgggct gaaggctacc	300
tttgc当地tgc acaggctccc tccttgcacg ctgggtccag tgccggccct ggcttc当地	360
gaataccctct ttgagggttga tgctacggcg ctgggtccag gacactcaac cccagacaat	420
gttgccggacg tggcgtggt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc	480
caggctgccc ggctgtccctg cctcggttctt gagggcatgg atcgtgtggg gggaaagact	540
ctgagcgtac aatcgggtcc cggcaggacg actatcaatg acctcggcgc tgc当地ggatc	600
aatgacagca accaaagcga agtattcaaa ttatttggaaa gatttcattt ggagggcgag	660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtaacaac cactacagct	720
ccttatggtg attccctggt aggccacaattt ccatcttgc atgagacctc tgc当地gtgt	780
agaatacagt cgctgactcc acatcgccca gctgagcggag gaggttgcaa gtgc当地tcgc	840
ggaactcctt cccgcatggt ctcagctgat cgaagagcat agtcttgc当地 accccaaggc	900
gagccctcaa gcgaaggcgc tcgacagtgt gagcttcgca cactactgt agaaggatct	960
aaacttgcct gctgttctcg gcgtggcaaa ccagatcaca cgc当地ctgc tcgggtgg	1020
agccccacgag atcagcatgc ttttctcac cgactacatc aagagtgc当地 ccggctc当地	1080
taatattgtc tcggataaga aagacggtg gcagtatatg cgatgc当地aaa caggtgc当地	1140
tgggtttctc tcagtggag actcggttct tagtggtcat tccaggatgc cagtc当地cttt	1200
gccatgccat gtc当地aggaa ctgttccag gctcagtgca cctcaacacc cccgtcgccg	1260
aaatttagca gtc当地catcc ggctgtacag tacgatcggc ctgggc当地gc gtgttccgaa	1320
gtaaaaaggt ggtggttcg ttaccgacaa cttgtatcc caccttgc当地 ttttaccac	1380
ctcttccgc cgagaagcaa gcattggctg aaaaatccat cctgggctac tatagcaaga	1440
tagtcttcgt atgggacaag ctgtggtgcc gc当地acaagg cttctcggc gtc当地tccat	1500
cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtc当地 cggcaatgg	1560
ccattacctg tttcatggtc ggagacccgg gacggaaatgc gtcccaacag tccaaggcagg	1620
tacgacagaa gtc当地tctgg aaccaactcc ggc当地ggctta cgagaacgcc ggggccc当地ag	1680
tcccaaggcc ggccaaacgtg ctc当地gatcg agtggtc当地a gc当地cgtat ttccaaggag	1740
cggccgagcgc cgtctatggg ctgaactgta tcaacacact gggttccggc ctc当地agaacgc	1800

cgttcaaggg tggcatttc gttggAACGG agacgtcttt ggTTTggaaa gggtatATgg 1860
aaggggccat acgatcggt cagcgaggcg ctgcagaagt tgtgccttagc ctgggccag 1920
cagcatag 1928

<210> 46

<211> 591

<212> PRT

<213> Rhinocladiella atrovirens

<400> 46

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Ala Ser Pro Ala
1 5 10 15

Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val Thr
20 25 30

Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro Ala
35 40 45

Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu
Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu
50 55 60

Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr
65 70 75 80

Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu
85 90 95

Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro
100 105 110

Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr
115 120 125

Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val Val
130 135 140

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln

145 150 155 160

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
165 170 175

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe
195 200 205

Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
210 215 220

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro
225 230 235 240

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
245 250 255

Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp
260 265 270

Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala
275 280 285

His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala
290 295 300

Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
305 310 315 320

Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
325 330 335

Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
340 345 350

Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
355 360 365

Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
370 375 380

Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys
385 390 395 400

Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu
405 410 415

Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser
420 425 430

Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser
435 440 445

Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr
450 455 460

Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp
465 470 475 480

Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val
485 490 495

Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro
500 505 510

Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe
515 520 525

Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
530 535 540

Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
545 550 555 560

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
565 570 575

Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala
580 585 590

<210> 47

<211> 600

<212> PRT

<213> Exophiala spinifera

<400> 47

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala
225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile

420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590

Val Ala Ser Leu Val Pro Ala Ala
595 600

<210> 48

<211> 1392

<212> DNA

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteine 461

<220>

<221> CDS

<222> (1)..(1392)

<223>

<400> 48
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 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt 96
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat 192
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag 336
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg 384
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag 432
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac 480
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc 528
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu

165	170	175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttc ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180	185	190	576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195	200	205	624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 210	215	220	672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225	230	235	720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245	250	255	768
ggc gcc gtg ttc cga agc aaa aag gtc gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260	265	270	816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275	280	285	864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290	295	300	912
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305	310	315	960
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325	330	335	1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340	345	350	1056
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355	360	365	1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370	375	380	1152
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385	390	395	1200

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag 1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt 1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 49

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteine 461

<400> 49

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
85 90 95

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
450 455 460

<210> 50

<211> 1392

<212> DNA

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<220>

<221> CDS

<222> (1)..(1392)

<223>

<400> 50

aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt	48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cggt ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggg gtt gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc	672

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala			
210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc			720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg			768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc			816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa			864
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa			864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc			912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc			960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac			1008
Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
325	330	335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga			1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
340	345	350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg			1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
355	360	365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag			1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
370	375	380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa			1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt			1248
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt			1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag			1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt			1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			

435

440

445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
450 455 460

<210> 51

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
85 90 95

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
450 455 460

<210> 52

<211> 1392

<212> DNA

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 169, 359, and 461

<220>

<221> CDS

<222> (1)..(1392)

<223>

<400> 52
aaa gac aac gtt gcg gac gtc gta gtg gtg ggc gct ggc ttg agc ggt 48
Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctc gtt 96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg			144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser			
35	40	45	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat			192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			
50	55	60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg			240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			
65	70	75	80
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa			288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln			
85	90	95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag			336
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			
100	105	110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg			384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
115	120	125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag			432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
130	135	140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac			480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
145	150	155	160
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc			528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
165	170	175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc			576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc			624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
195	200	205	
ggg caq tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc			672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala			
210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc			720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg			768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260 265 270	816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285	864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Ser Lys Ile Val Phe 290 295 300	912
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320	960
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335	1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340 345 350	1056
cg ^g aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355 360 365	1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 375 380	1152
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385 390 395 400	1200
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 405 410 415	1248
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 420 425 430	1296
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 435 440 445	1344
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 450 455 460	1392

<210> 53

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 169, 359, and 461

<400> 53

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
85 90 95

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile

→

180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225 230 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305 310 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385 390 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
450 455 460

<210> 54

<211> 11

<212> PRT

<213> Exophiala spinifera

<400> 54

Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10